

ES  
Subsequently, an End Rescue Site was ligated into the EcoRI site. Hereto, two oligonucleotides (strand 1: 5'-TTCGGATCCGGTACCATCGAT-3' (SEQ ID NO:161) AND STRAND 2: 3'GCCTAGGCCATGGTAGCTATT-5' (SEQ ID NO:162) were ligated into a partial (dATP) filled ECORI site, generating the vector pDF1. Triplet repeat containing fragmentation vectors were constructed by cloning of a 21bp and a 30bp CAG/CTG adapter into the Klenow-filled PstI site of pDF1. Transformation and selection resulted in a (CAG)<sub>7</sub> and a (CTG)<sub>10</sub> fractionation vector with the orientation of the repeat sequence 5' to 3' relative to the telomere.

### Remarks

Applicants file a substitute Sequence Listing herewith to correct the inadvertent omission of sequences from the previously filed Sequence listing. Applicants have also amended the specification to include sequence identification numbers that were inadvertently omitted from the application as originally filed. No new matter has been added.

Applicants respectfully request reconsideration of the specification in view of the amendments made above. If the Examiner wishes to advance the prosecution, or if the amendment is defective or unclear in some way, then the Examiner is invited to telephone the undersigned at the telephone number listed below.

Respectfully submitted,

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**X08/01/02**

**Marked-up Specification**

**Page 22, line 23 through Page 23 line 20:**

FIGURE 1 shows a sequence of nucleotides which is the left arm end-sequence of YAC 766\_f\_12; {(SEQ ID NO: 1).}

FIGURE 2 shows a sequence of nucleotides which is a right arm end-sequence of YAC 766\_f\_12; {(SEQ ID NO: 2).}

FIGURE 3 shows a sequence of nucleotides which is the left arm end-sequence of YAC 717\_d\_3; {(SEQ ID NO:3).}

FIGURE 4 shows a sequence of nucleotides which is the right arm end-sequence of YAC 717\_d\_3; {(SEQ ID NO:4).}

FIGURE 5 shows a sequence of nucleotides which is the right arm end-sequence of YAC 731\_c\_7; {(SEQ ID NO:5).}

FIGURE 6 shows a sequence of nucleotides which is the left arm end-sequence of YAC 752\_g\_8; {(SEQ ID NO:6).}

FIGURE 7 shows a sequence of nucleotides which is the left arm end-sequence of YAC 942\_c\_3; {(SEQ ID NO:7).}

FIGURE 8 shows a sequence of nucleotides which is the right arm end-sequence of YAC 942\_c\_3; {(SEQ ID NO:8).}

FIGURE 9 shows a sequence of nucleotides which is the left arm end-sequence of YAC 961\_h\_9; {(SEQ ID NO:9).}

FIGURE 10 shows a sequence of nucleotides which is the right arm end-sequence of YAC 961\_h\_9; {(SEQ ID NO:10).}

FIGURE 11 shows a sequence of nucleotides which is the left arm end-sequence of YAC 907\_e\_1; {(SEQ ID NO:11).}

Page 23, line 35 through page 24, line 26:

FIGURE 15 shows (a) a CAG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 961\_h\_9 {(SEQ ID NO:12)}. The sequence in italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence {(SEQ ID NOs:13 and 14)}.

FIGURE 16 shows (a) a CAG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 766\_f\_12 {(SEQ ID NO: 15)}. The sequence in italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence {(SEQ ID NOs:16 and 17)}.

FIGURE 17 shows (a) a CAG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 766\_f\_12 {(SEQ ID NO: 18)}. The sequence in italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence {(SEQ ID NOs: 19 and 20)}.

FIGURE 18 shows (a) a CTG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 907\_e\_1 {(SEQ ID NO: 21)}. The sequence in italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence {(SEQ ID NOs:22 and 23)}.

**Page 36 line 1 through Page 61 line 22:**

D18S60:

Database ID: AFM178XE3 (Also known as 178xe3, Z16781, D18S60)  
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs  
Chromosome: Chr18

Primers:

Left = CCTGGCTCACCTGGCA {(SEQ ID NO:24)}  
Right = TTGTAGCATCGTTGTAATGTTCC {(SEQ ID NO:25)}  
Product Length = 157

Review complete sequence:

AGCTATCCTGGCTCACCTGGCAAAAATACAGTGTATACACACACACACACACAC  
ACACACACACACAGAGTGTNTTANTNATTCCAGCAAATAATATTACATATAAAAGA  
TCTAATTGGTTCATCATGTAAATTTAGTAGGAACATTACAACGATGCTACAAGANTT  
TATCCAAAAGTGAATTTCTTAGAATATCTGTTAAAAGTAATTTTATTTCAGTTAATA  
GAAATTCTATTGAAAACATCAAACCTATAAAGCT {(SEQ ID NO:26)}

Genbank ID: Z16781

Description: H. sapiens (D18S60) DNA segment containing (CA) repeat; clone  
Search for GDB entry

WI-9222:

Database ID: UTR-03540 (Also known as G06101, D18S1033, 9222, X63657)  
Source: WICGR: Primers derived from Genbank sequences  
Chromosome: Chr18

Primers:

Left = GATCCCATAAAGCTACGAGGG {(SEQ ID NO:27)}  
Right = GAGTCTAAAGACAAGAAAGCATTGC {(SEQ ID NO:28)}  
Product Length = 99

Review complete sequence:

TCTTCTTACCCCTTGGAAGAAGACTGTTTCCAAATAATTTGAACAGCTTGCTGCTAA  
ATGGGACCCAATTTTTGGCCTATAGACACTTATGTATTGTTTTCGAATACGTCAGATT  
GGACCAGTGCTCTTCAGGAATGTGGCTGCAAGCAAGGGGCTAGAAGTTCACCTCCT  
GACAGTATTATTAATACTATGCAAATATGGAATAGGAGACCATTTGATTTTCTAGGC  
TTTGTGGTAGAGAGGTGAAGGTATGAGAATTAATAGCGTGTGAACAAAGTAAAGAA  
CAGGATTCCAGAATGATCATTAAATTTGTTTCTATTTATTCTTTTTTGCCCCCTAGA  
GATTAAGTCCAGAAATGTACTTTCTGGCACATAAAGAAATCTTGAGGACTTTGTTTA  
AACCTTCCATAAAAAACAATTTTCGGTTTCTCGGGTNNNNNNNNNNNNNNNNNNNN  
NNNTTCTTTCTTTG  
TGTATTTTATTCAAGATGAGTTGGACCCATTGCCAGTGAGTCTGAATGTCACTGACA  
GCCCTGTGTTGTGCTCAGGACTCACTCTGCTGCTGGTGGAACTCATGGCTTCTCTCT  
CTCTTTGATCCCATAAAGCTACGAGGGGGACGGGAGAGGGCAGTGCAATGGGAAGT  
AAAGAGATATTTTCCAGTAGGAAAAGCAATGCTTTCTTGTCTTTAGACTCAAATGCT  
TAGGGAACGTTTCATTTCTCATTTCATGGGGAAAGGCAGCCTCCTTAAATGTTTTCTG  
AAGAGCGGTAAATCTAGAAGCTTAAGAATTTACAGTTCCTTCAATAACCATGATGA  
CCTGAAGTTCACCTATCCCATTTTAGCATCTACTTGTTTTTCCCATCTCTTCCTTTCCA

ATTTTGCTTATACTGCTGTAATATTTTGTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNG  
ACCAGCTAAAATTTTCGACTTGACTTTTTAACTTAACTCATGAATTAATTAAAGCAA  
ATGAAAAAATTAAAAAGTGTGACTTTTTCTCGGAGCATATATGTAGCTTTTAGGAAA  
GGCTGATGATGGTATAAAGTTTGCTCATTAAGAAAAAAGACAAGGCTGATTTTGA  
AGAGAGTTGCTTTTGAAATAAAATGATCA {(SEQ ID NO:29)}

Genbank ID: X63657

Description: H.sapiens fvt1 mRNA

Search for GDB entry

WI-7336:

Database ID: UTR-04664 (Also known as PI5, G00-679-135, G06527, 7336, U04313)

Source: WICGR: Primers derived from Genbank sequences

Chromosome: Chr18

Primers:

Left = AGACATTCTCGCTTCCCTGA {(SEQ ID NO:30)}

Right = AATTTTGACCCCTTATGGGC {(SEQ ID NO:31)}

Product Length = 332

Review complete sequence:

TAAGTGGCATAGCCCATGTAAAGTCCTCCCTGACTTTTCTGTGGATGCCGATTTCTGT  
AAACTCTGCATCCAGAGATTCATTTTCTAGATACAATAAATTGCTAATGTTGCTGGA  
TCAGGAAGCCGCCAGTACTTGTCAATATGTAGCCTTCACACAGATAGACNNNNNNN  
NNNNCCAATTCTATCTTTTGTTCCTTTTTTCCCATAAGACAATGACATACGCTTTTA  
ATGAAAAGGAATCACGTTAGAGGAAAAATATTTATTCATTATTTGTCAAATTGTCCG  
GGTAGTTGGCAGAAATACAGTCTTCCACAAAGAAAATTCCTATAAGGAAGATTTG  
GAAGCTCTTCTTCCCAGCACTATGCTTTCCTTCTTTGGGATAGAGAATGTTCCAGACA  
TTCTCGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCC  
CTGGCTCCAGTGAAACTTGGGCACATGCTCAGGCTACTATAGGTCCAGAAGTCCTTA  
TGTTAAGCCCTGGCAGGCAGGTGTTTATTAATAAATTCTGAATTTTGGGGATTTTCAA  
AGATAATATTTTACATACACTGTATGTTATAGAAGTTCATGGATCAGATCTGGGGCA  
GCAACCTATAAATCAACACCTTAATATGCTGCAACAAAATGTAGAATATTCAGACA  
AAATGGATACATAAAGACTAAGTAGCCCATAGGGGTCAAAATTTGCTGCCAAATG  
CGTATGCCACCAACTTACAAAAACACTTCGTTTCGCAGAGCTTTTCAGATTGTGGAAT  
GTTGGATAAGGAATTATAGACCTCTAGTAGCTGAAATGCAAGACCCCAAGAGGAAG  
TTCAGATCTTAATATAAATTCATTTTCTATGATAGCTGTCCCATCTGGTCATGTG  
GTTGGCACTAGACTGGTGGCAGGGGCTTCTAGCTGACTCGCACAGGGATTCTCACA  
TAGCCGATATCAGAATTTGTGTTGAAGGAAGTGTCTCTTCATCTAATATGATAGCG  
GGAAAAGGAGAGGAACTACTGCCTTTAGAAAATATAAGTAAAGTGATTAAAGTGC  
TCACGTTACCTTGACACATAGTTTTTTCAGTCTATGGGTTTAGTTACTTTAGATGGCAA  
GCATGTAAGTTATATTAATAGTAATTTGTAAAGTTGGGTGGATAAGCTATCCCTGTT  
GCCGGTTCATGGATTACTTCTCTATAAAAAATATATATTTACCAAAAAATTTTGTGA  
CATTCCTTCTCCCATCTCTTCTTCTGACATGCATTGTAAATAGGTTCTTCTTGTCTGAG

ATTCAATATTGAATTTCTCCTATGCTATTGACAATAAAATATTATTGAACTACC  
{(SEQ ID NO:32)}

Genbank ID: G06527

Description: WICGR: Random genome wide STSs

X

WI-8145:

Database ID: EST102441 (Also known as D18S1234, G00-677-827, G06845, 8145, T49159)

Source: WICGR: STSs derived from dbEST sequences

Chromosome: Chr18

Primers:

Left = GAAATGCACATAACATATATTTGCC {(SEQ ID NO:33)}

Right = TGCTCACTGCCTATTTAATGTAGC {(SEQ ID NO:34)}

Product Length = 184

Review complete sequence:

GTTGTTTGGANGCAGGTTTATTTATTATATACTTGCAATTGAATATAAGATACAGAC  
ATATATATGTGTTATGTATTTCTAGAAATGCACATAACATATATTTGCCTATTGTTTA  
ATGTTTTTTCCAGANATTTATTACAGAAGGGCATGGAGGGATACCTACTTATTCTTC  
ATTATGAGAACAATTAAAGGCATTTATTAGATAGGAAATTAACAGANCATCTGCTTC  
TATAACTTTATTAGCTACATTAAATAGGCAGTGAGCANTAATTTAAANCTCACCAT  
TATATAAANTANTAAATACCAAAGTAAAAG {(SEQ ID NO:35)}

\_\_\_\_\_ : left and right primer

PCR Conditions

Genbank ID: T49159

Description: yb09e07.s1 Homo sapiens cDNA clone 70692 3' similar to gb:J02685

UniGene Cluster Description: Human mRNA for Arg-Serpin (plasminogen activator-inhibitor 2, PAI-2) Search for GDB entry

WI-7061:

Database ID: UTR-02902 (Also known as PAI2, G00-678-979, G06377, 7061, M18082)

Source: WICGR: Primers derived from Genbank sequences

Chromosome: Chr18

Primers:

Left = TGCTCTTCTGAACAACTTCTGC {(SEQ ID NO:36)}

Right = ATAGAAGGGCATGGAGGGAT {(SEQ ID NO:37)}

Product Length = 338

Review complete sequence:

AACTAAGCGTGCTGCTTCTGCAAAAGATTTTTGTAGATGAGCTGTGTGCCTCAGAAT  
TGCTATTTCAAATTGCCAAAAATTTAGAGATGTTTTCTACATATTTCTGCTCTTCTGA  
ACAACTTCTGCTACCCACTAAATAAAAAACACAGAAATAATTAGACAATTGTCTATTA  
TAACATGACAACCCTATTAATCATTGGTCTTCTAAAATGGGATCATGCCCATTTAG  
ATTTTCCTTACTATCAGTTTATTTTTATAACATTAACCTTTTACTTTGTTATTTATTATT  
TATATAATGGTGAGTTTTAAATTATTGCTCACTGCCTATTTAATGTAGCTAATAAAGT  
TATAGAAGCAGATGATCTGTTAATTTCTATCTAATAAATGCCTTTAATTGTTCTCAT  
AATGAAGAATAAGTAGGTATCCCTCCATGCCCTTCTATAATAAATATCTGGAAAAAA  
CATTAAACAATAGGCAAATATATGTTATGTGCATTTCTAGAAATACATAACACATAT  
ATATGTCTGTATCTTATATTCAATTGCAAGTATATAATAAATAAACCTGCTTCCAAAC  
AACNNNNNNNNNNNNNNNGGAATTC {(SEQ ID NO:38)}

#### PCR Conditions

Genbank ID: G06377

Description: WICGR: Random genome wide STSs

#### D18S68:

Database ID: AFM248YB9 (Also known as 248yb9, Z17122, D18S68)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

#### Primers:

Left = ATGGGAGACGTAATACACCC {(SEQ ID NO:39)}

Right = ATGCTGCTGGTCTGAGG {(SEQ ID NO:40)}

Product Length = 285

Review complete sequence:

AAAGAGTTGGGGTTGTGAATTCCACACACAGTCAACTATTGGCTATGGGCTTACCAT  
GGGAGACGTAATACACCCGGNACTTCCAACCTCACATACCAGAGACATGGCTCTAGC  
ACCCAATGGAAATATGCTGAATGTTGCAGGTGCAAGACAGCAACAAAGCAGACAGA  
GGCACATAGACAAGGCACCAACAGTGTCCACTATACCCTGACAGTGTGGAAAGTTG  
TAGATAGGATGAAGAGAAAGAATACACACACACACACACACACACACACACAC  
ACACACACACACACCGGTAGANACTTACTACNCAAAGTGTGANCCTCAGACCAGC  
AGCATCTGGCNAAATGGTGATCTATCACCTTCCAG {(SEQ ID NO:41)}

Genbank ID: Z17122

Description: H. sapiens (D18S68) DNA segment containing (CA) repeat; clone

WI-3170:

Database ID: MR3726 (Also known as D18S1037, G04207, HALd22f2, 3170)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

## Primers:

Left = TGTGCTACTGATTAAGGTAAAGGC {(SEQ ID NO:42)}

Right = TGCTTCTTCAATTTGTAGAGTTGG {(SEQ ID NO:43)}

Product Length = 156

Review complete sequence

CTGAGACAAGGCAGGCAAACAACCTCTAAAAATCTACAATTGGTGATTGGTGTGCT  
ACTGATTAAGGTAAAGGCACAGAATTATACATCCAGGTTNCTATTACTTATGGCAGA  
CTCAGGACCCAGGTTNAGAGACCACTGGCCTTAAGAAAAAAAAAATGGGGTTCCTGAT  
TTCTGGATAATAATCCAACTCTACAAATTGAAGAAGCAACATACCCTCTTTGTTA  
{(SEQ ID NO:44)}

Genbank ID: G04207

Description: WICGR: Random genome wide STSs

WI-5654:

Database ID: MR10908 (Also known as D18S1259, G00-678-695, G05278, 5654)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

## Primers:

Left = CTTAATGAAAACAATGCCAGAGC {(SEQ ID NO:45)}

Right = TGCAAAATGTGGAATAATCTGG {(SEQ ID NO:46)}

Product Length = 149

Review complete sequence:

CTACAAAATGCATGTGGCTTTGGCTTTGAAATAGTACACCCTATCAAAGACTAAATT  
TTCTTAATGAAAACAATGCCAGAGCTTTTTTCATGATATTTTGTTTTATAGAGATGGGG  
AACAATCTGGACGTTGTTTCCTTATCTGGGTGGTAATCGAGGCTTAGCAATTTCCCA  
CAGCGTTACACAAATCCAGATTATTCCACATTTTGCAAATA {(SEQ ID NO:47)}

Genbank ID: G05278

Description: WICGR: Random genome wide STSs

D18S55:

Database ID: AFM122XC1 (Also known as 122xc1, Z16621, D18S55, GC378-D18S55)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

## Primers:

Left = GGGAAGTCAAATGCAAAATC {(SEQ ID NO:48)}

Right = AGCTTCTGAGTAATCTTATGCTGTG {(SEQ ID NO:49)}



Product Length = 143

Review complete sequence:

AGCTGAACATGCCTTTTCATGGAGCAGTTTCNAAATACACTTTTGGTACAATCTGCA  
GGTGGATATTTGGAGCTCAGGAGTTTGAGACCAGCCTGGGCAACATGGTGAAATCC  
CGTCTCTACTAAAATACAAAAAATTAGCCAGGTGTGGCGGCATGTGCCTGTAGNCCC  
AGGATGGATTGAGTGGGTGAGATATGGAATAAGTGGTGGGAAGTCAAATGCAAAAT  
CAATTCAGTTTGTCAATATTGATTCTCTATTCTAGCCTGGCGTGGTTTTTCCTCGTCA  
CAGCATAAGATT  
ACTCAGAAGCT {(SEQ ID NO:50)}

Genbank ID: Z16621

Description: H. sapiens (D18S55) DNA segment containing (CA) repeat; clone

#### D18S969:

Database ID: GATA-P18099 (Also known as G08003, CHLC.GATA69F01,  
CHLC.GATA69F01.P18099)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats  
Chromosome: Chr18

Primers:

Left = AACAAGTGTGTATGGGGGTG {(SEQ ID NO:51)}

Right = CATATTCACCCAGTTTGTGTC {(SEQ ID NO:52)}

Product Length = 365

Review complete sequence:

CAGGGAAATGCAAATCAAAACCACAATGAGTTATCTCCTCATACCTTTAATGATGGC  
TAATATTAAACAAGAGATAACAAGTGTGTATGGGGGTGTGGAGAAAAGAGAATGTN  
CGAACACTCTTGGTTGAAATATAAGTTGGTAGANCCATTATGCAAAACAGTATGAAT  
CTTTATCAGTATAANATTAGGACCTNGCATATGATCNCAGCAATCNCCACNTCTGNG  
NGATCNCACNCNCTATCTCTCTATATCTATCTATCTATCTATCTATCTATCTATCTATCT  
TATCTATCTATCTATCTATCTGTCTGTCTATCATCTATCTATCTTCTATCTATCTATCT  
ATCTTTCTATCTATCTATCTGTCTATCTATNCCGGAATATTTTTCAGCCATNNAATA  
AGGAAGTCCTGCTATTTGCAACAAACTGGGTGAATATGGAGAACGTTATGCTAAAT  
GCAATATGCTAAAGACAGACACAGAAAGACAAGTATGACCTCACTTATATGTGGAA  
ACTGAAAAAGCCATACTCATTACAGCAAAGAGTAGAATGTTGGTTACCAGGGGCAA  
AGAGGGTAGAAATGAGGGGAGTGAGAAAATGTCAATCAAAGTGTAAGAATGTTATA  
ACATAAATAAATTCATAGAG {(SEQ ID NO:53)}

Genbank ID: G08003

Description: human STS CHLC.GATA69F01.P18099 clone GATA69F01.

#### D18S1113:

Database ID: AFM200VG9 (Also known as D18S1113, 200vg9, w2403)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = GTTGACTCAAGTCCAAACCTG {(SEQ ID NO:54)}

Right = CAAAGACATTGTAGACGTTCTCTG {(SEQ ID NO:55)}

Product Length = 207

Review complete sequence:

AGCTGCATATAAACTATTCCATTTTCACATTTTTGAAGACATTTGTAGCCATGATACT  
TTGCTGTTGTCTGTGGGCCACCTCTTTTTGAAGTGTGTAGTTAACTGTGCTCCTGTAA  
TCTGTTGTCTGTTGACTCAAGTCCAAACCTGTTCTGCGTGGCATGTTTCTNCAACTTG  
ATGTGATGCTATTTATCACTTTCTTTGAAGTTAAGTCTCTATGTCTTTGTATTCTTTCT  
GTGTACCCAGGGATATGTTTGTGCATGCACACGCATAAACACACACACACACACAC  
ACACACACAGAGACAGAGACAGAGAACGTCTACAATGTCTTTGTGAG {(SEQ ID  
NO:56)}

D18S868:

Database ID: GATA-D18S868 (Also known as G09150, CHLC.GATA3E12,  
CHLC.GATA3E12.496, CHLC.496, D18S868)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats

Chromosome: Chr18

Primers:

Left = AGCCAATACCTTGTAGTAAATATCC {(SEQ ID NO:57)}

Right = GATTCTCCAGACAAATAATCCC {(SEQ ID NO:58)}

Product Length = 189

Review complete sequence:

GAGTGAGCCAATACCTTGTAGTAAATATCCATCTATCTTTGATGTATCTATGTATCTA  
TCTTTGTATCTATATGTCTATGTATCTATGTATGTATGTATCTATCTATCATCTATCTA  
TCTATCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCCNTTTGGG  
ATTATTTGTCTGGAGAATCCTGATTAACATAGTCTGCTAACTTTTATCTGTATCTCCT  
ATGTGTATGCTTCTCCTTCTTCCTGTCTCTCTCTCTTCTTTGTCCTCATTTAANCTCCTT  
TCCTGGGNATATTGGNAATTTTGATTGGANTCTGGACANTGTAGGAGTAAAAATTT  
{(SEQ ID NO:59)}

Genbank ID: G09150

Description: human STS CHLC.GATA3E12.P6553 clone GATA3E12.

WI-9959:

Database ID: MR12816 (Also known as D18S1251, G00-678-524, G05488, 9959)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

## Primers:

Left = TGCCAACAGCAGTCAAGC {(SEQ ID NO:60)}

Right = AGCACCTGCAGCAGTAATAGC {(SEQ ID NO:61)}

Product Length = 110

Review complete sequence:

CtggtttatttgaaaaaaaatctgtctccaagaagaaagttcattctACCTGTTGCCAACAGCAGTCAAGCGGA  
CATGTTTAAAATTTTTTAAAAAAGTATTTTTTTTCCAACTGGNGTTTAATAGCCTCA  
TTTTGGCTTTTGCTATTACTGCTGCAGGTGCTTTNATTTTTTTCCTCTGCATTATAATT  
AC {(SEQ ID NO:62)}

Genbank ID: G05488

Description: WICGR: Random genome wide STSs

Search for GDB entry

D18S537:

Database ID: CHLC.GATA2E06.13 (Also known as CHLC.13, GATA2E06, D18S537, GATA-D18S537)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats

Chromosome: Chr18

## Primers:

Left = TCCATCTATCTTTGATGTATCTATG {(SEQ ID NO:63)}

Right = AGTTAGCAGACTATGTTAATCAGGA {(SEQ ID NO:64)}

Product Length = 191

Review complete sequence:

AAAGCTGAGTGAGCCAATACCTTGTAAGTAAATATCCATCTATCTTTGATGTATCTAT  
GTATCTATCTTTGTATCTATATGTCTATGTATCTATGTATGTATCTATCTATCAT  
CTATCTATCTATCATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCC  
NTTNGGTATTATTNGTCTGGNGAATCCTGATTAAACATAGTCTGCTAACTTNTATCTGT  
ATCTNCTATGTGTATGCTTCTNCTTCTTCTGTCTCTCTCTGCTTTGTCTCAATTN  
AAATCTCC {(SEQ ID NO:65)}

Genbank ID: G07990

Description: human STS CHLC.GATA2E06.P6006 clone GATA2E06.

Search for GDB entry

D18S483:

Database ID: AFM324WC9 (Also known as 324wc9, Z24399, D18S483)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

## Primers:

Left = TTCTGCACAATTTC AATAGATTC {(SEQ ID NO:66)}

Right = GAACTGAGCAAACGAGTATGA {(SEQ ID NO:67)}

Product Length = 214

Review complete sequence:

AGCTCTGCTGGAAGAGCAGGGCTGTTTTCTGCACAATTTCAATAGATTCCCCTACCC  
TGGGTTTTTCAGTAGATAGATAGATAGATGATAGATAGGTAGATAGATAGATAGAT  
AGATAGATAGATAGATAGATAGATGATAGATAGATTTTATATATAGTATATAAAATC  
TACACACACACACACACACACACACACATATTTGCCTTTCCTTGACTATCATACT  
CGTTTGCTCAGTTCTTTTTTTTTTTAAATTTTGTGTTGTAAATCCAAAATGCTT {(SEQ  
ID NO:68)}

Genbank ID: Z24399

Description: H. sapiens (D18S483) DNA segment containing (CA) repeat; clone

Search for GDB entry

#### D18S465:

Database ID: AFM260YH1 (Also known as 260yh1, Z23850, D18S465)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = ATATTCCCCTATGGAAGTACAG {(SEQ ID NO:69)}

Right = AAAGTTAATTTTCAGGCACTCT {(SEQ ID NO:70)}

Product Length = 232

Review complete sequence:

AGCTCTGTCCCTCTAGAGAACGCTGACTAATATATTCCCCTATGGAAGTACAGATGG  
TTTTNTAAATAAATTTATCTGATTGTGATGAGATAATCATCATTTTTATGTTTCAGT  
GTTTTCTAAATTTTTATTGTTATTGTTTTTATACTCTAAATGGTTTTTAAATATGCA  
CATATGTGCATATTTTACACACACACACACACACACACTCTCTTTATTTAGAA  
GCATTATAGATAGAGTGCCTGAAAATTAACCTTTTAACCNAAGAAAAGACAATAAGG  
AACAATAGGGAAGTTATCCTTTGCTAAGGGTATGGAAAATATTCACATATTATTTAT  
AACANGTTAAACCAAGTCATGCTTGANTATAATAGCT {(SEQ ID NO:71)}

Genbank ID: Z23850

Description: H. sapiens (D18S465) DNA segment containing (CA) repeat; clone

Search for GDB entry

#### D18S968:

Database ID: GATA-P34272 (Also known as G10262, CHLC.GATA117C05,  
CHLC.GATA117C05.P34272)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats

Chromosome: Chr18

Primers:



## Primers:

Left = TCCTCTCATCTCGGATATGG {(SEQ ID NO:78)}

Right = AAGGCTTTCAGACTTACACTGG {(SEQ ID NO:79)}

Product Length = 394

Review complete sequence:

TTATTTATTCACTCATTCAATAAATATTTATGAATTCCTTTAATGGCNANGAAAGTA  
TGTTTGGTACTGAATATGGTGAGCAAGATTTTCCTCTCATCTCGGATATGGAAAGAT  
CTTGAAATCATTATACNTCATACTTACAATANGAAAGAAGCTGAGCAATTTGAAA  
ATCAACAATTTCTTTTGTACNTGTCAGAAAAGTGAAGATATATTAATCAGGGTTCTT  
CAGAGAAACATAACCAATAGGNCACAGNTCTATATGNCCNCNTTTATCTATCTATCT  
ATCTATCTATCNCTATCTATCNANACCNGGNGAANTNATNTTTGNGAGATTNATGC  
AAGNCTGAGAAANACCNAAGAANCTGCTCCCTGTNAACTNGAGATNCAAGAANCT  
GAANAGTATAGNTCCAGTCCNAAGTCTANAGACCTTAGAATTAGGAAAAGTATAC  
TATAAATACCAAGTGTAAGTCTGAAAGCCTTAAANACCANATAGTGCCATTGAAAGG  
GCAGAAGACTGATGTCCAGTTCAAGCAGGCAAAGTTAGAGAAGCCTTATTTTCTGC  
AACATTGTTCTATTCAGACCCTTNANANGATTGACNATGTCCACCCA {(SEQ ID  
NO:80)}

Genbank ID: G08001

Description: human STS CHLC.GATA52H04.P16177 clone GATA52H04.

Search for GDB entry

WI-2620:

Database ID: MR1436 (Also known as G03602, D18S890, HHAa12h3, 2620)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

## Primers:

Left = TCTCCAAGCTATTGATTGGATAA {(SEQ ID NO:81)}

Right = TTAAGAGCCAATTTATATAAAAGCAGC {(SEQ ID NO:82)}

Product Length = 177

Review complete sequence:

CCCCTTTTGCCAACGCCATGCTTCACGTAGGGAGCCTGACATGCAGAAAAGTCTCCA  
AGCTATTGATTGGATAAAGAGCCAGAGCTGACTGAATTCCATTCTTCTTGAGCCTCT  
CATTCTGTGTTTCTCGAATTTTACCAAAGCATCTTGACACACAAATATCTGACTCAA  
GGAAAAGGAAAAACAACTGCTTTTCTCCAGCTGCTTTTATATAAATTGGCTCTTAA  
ACTTTCTAAGTTTATTATGGATA {(SEQ ID NO:83)}

Genbank ID: G03602

Description: WICGR: Random genome wide STSs

Search for GDB entry

WI-4211:

Database ID: MR6638 (Also known as G03617, D18S980, 4211)  
Source: WICGR: Random genome wide STSs  
Chromosome: Chr18

Primers:

Left = ATGCTTCAGGATGACGTAATACA {(SEQ ID NO:84)}

Right = AAATTCTCGCTGATTGGAGG {(SEQ ID NO:85)}

Product Length = 113

Review complete sequence:

CTAGTACCATAATCCCTTTTGGGAATAAACCATCCCACCTTTAGTCAGANCAGATGCT  
TCAGGATGACGTAATACATAATAAGCCTACTCAGTTCTACTCTGGCTTTGTATGTCTT  
CAAAGTGATATTTTTTAAGTATTACTTGTCCCTCCAATCAGCGAGAATTT {(SEQ ID NO:86)}

Genbank ID: G03617

Description: WICGR: Random genome wide STSs

Search for GDB entry

D18S876:

Database ID: GATA-D18S876 (Also known as G09963, CHLC.GATA61E10, D18S876)  
Source: CHLC: genetically mapped polymorphic tetranucleotide repeats  
Chromosome: Chr18

Primers:

Left = TCAAACCTTATAACTGCAGAGAACG {(SEQ ID NO:87)}

Right = ATGGTAAACCCTCCCCATTA {(SEQ ID NO:88)}

Product Length = 171

Review complete sequence:

AAGACTGCAATTACATTTGCATCAAACCTTATAACTGCAGAGAACGTTGCCCACTATT  
TTATACCACACAACAGTATTCTTAGCCAGATTACATCTATCTATCTATCTATCT  
ATCTATCTATCTATCTATCTATCTATCATCTATCTAGCTAGCTATCTATCTATAGAAC  
TAATGGGGAGGGTTTACCATGTTTGGGTGAACCCAAACATTTTATGGNCAAGGGNTT  
GGAAAATTACCCTTATCTACAACNTTNAACTTGTTTTGGTAGGNGTGNTAATTCCN  
TGGGNTTGGGAANAACCTTTGNAATTCCTCNTTGTNTNTNATTNNNNATTNNTNNNC  
ATTATTNTGGGGTNTTCNGGGTGGAGGGCTNANTTTGGCCNCCCGGGTCCNNGGNG  
CNAGTNGGNNNGGNTNNTNGGGTTTNCCTGGGAANCNTNCCNCCTNCNGGGGNTTC  
ANGGGNTTTTNTTTNNTTG {(SEQ ID NO:89)}

Genbank ID: G09963

Description: human STS CHLC.GATA61E10.P17745 clone GATA61E10.

Search for GDB entry

GCT3G01:

Database ID: GCT-P10825 (Also known as G09484, CHLC.GCT3G01, CHLC.GCT3G01.P10825)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats  
Chromosome: Chr18

Primers:

Left = CTTTGCAATCTTAGTTAATTGGC {(SEQ ID NO:90)}

Right = GAACTATGATATGGAGTAACAGCG {(SEQ ID NO:23)}

Product Length = 128

Review complete sequence:

AGATGTTTAACTTTGCAATCTTAGTTAATTGGCAGAAATGAAATTTAGTTTCCACAA  
CTTTTATTCGATATTAACACACCACCACCATCAGCAGCAGCAGCAGCAGCAGCAGC  
ATCGCTGTTACTCCATATCATAGTTCAGAGCATTTAAAGNGGTCAAAATATACAAC  
AGGCTGACACCNGNATAAGGTTTAATTTTAAACCNGNGGTCTNCCCTCTAAGGNGG  
NTTTTTTTTTCTTGNCNTGGCTTCTTTTTCCNTTTGCTTTTGTAATAATCAAGGNATT  
TTTGGGTNTTCNTGGNANTTNNCANNANTNNTNNTTNNNCNCCCCCCTTTGNGG  
CGGGGGTCCCNNTTGCCCCGGGGTTGNGTGCAGTAGGGGGGTNCNCGGGTNNNGN  
AAGTTTNGGGGCCCT {(SEQ ID NO:91)}

Genbank ID: G09484

Description: human STS CHLC.GCT3G01.P10825 clone GCT3G01.

WI-528:

Database ID: MH232 (Also known as G03589, 528, D18S828)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

Primers:

Left = TTCTGCCTTTCCTGACTGTC {(SEQ ID NO:92)}

Right = TGTTTCCCATGTCTTGATGA {(SEQ ID NO:93)}

Product Length = 211

Review complete sequence:

CTACTAAGCAAATTCTGCTCAGCCTTCTGCCTTTCCTGACTGTCTTGTTGGCCCTTCC  
CACTTTAAGGATGCCTGTTTAAGTAGCCACCTCTAATTAGGAATCTTCCCTTGTTCTT  
TCTCAGGAGGCTTAGACACTGTCAGTTTCCTGAAGACAGAAAATAAGCCTGCATTAT  
CCTAGTAGTGGATTCAAACTAATTGTGTCCTGAGTCTTCAATCATCAAGACATGG  
GAAACACTCAACAG {(SEQ ID NO:94)}

Genbank ID: G03589

Description: WICGR: Random genome wide STSs

Search for GDB entry

25. WI-1783:



Database ID: MR432 (Also known as G03587, \_shu\_31.Seq, 1783, D18S824)

Source: WICGR: Random genome wide STSs

Chromosome: Chr18

Primers:

Left = CCAGTAATTAGACATTGACAGGTTC {(SEQ ID NO:95)}

Right = TTTTACTAGACAGGCTTGATAAACAA {(SEQ ID NO:96)}

Product Length = 305

Review complete sequence:

CCAGTAATTAGACATTGACAGGTTCCATACTAGTAATGTAGGGAATAGGGCTGCTGC  
TTTTTGGGTTTCCTTGAGTATACTTTGTGCTGCATAAATATGGCAATGGATAGTAAAT  
AATTTGTATGCAGACCTTTAGTGTGATTAACTGTGAATAAGGGAACAACAATCAA  
GGACAAAAATCAAAAGACTAATTCTCTATACATTTTGAGCTTTTGTAAGTAAGTAAG  
ATTAGCTGAATATATCTGAAAAATTTCTAATCTCCTTTACAATTTTAAATTTGTTTA  
TCAAGCCTGTCTAGTAAAAATAATTCAGTTTCGGAATGTGG {(SEQ ID NO:97)}

Genbank ID: G03587

Description: WICGR: Random genome wide STSs

Search for GDB entry

D18S477:

Database ID: AFM301XF5 (Also known as 301xf5, Z24212, D18S477)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = GGACATCCTTGATTTGCTCATAA {(SEQ ID NO:98)}

Right = GATTGACTGAAAACAGGCACAT {(SEQ ID NO:99)}

Product Length = 243

Review complete sequence:

GGACATCCTTGATTTGCTCATAATACACTCATTCCTTTCACCATTGAGTGTGCACATA  
TTTCTCTGATTGGAAAGAACTACAGAGGAGGTTTTACNTTTTACTTTCCAGTTTGCTA  
TTAAAGAGAGAGAAACTAACAGAGNGAAATCAAGCAACTCAAAACAACCTTACACAC  
ACACACACACACACACTCACAAAGATATTTTGTTTACCATATGTATTGATGTGCC  
TGTTTTCAGTCAATCCCACAGGAAGGGCTAAGGAGAGTGACATCTGGGCTACATTAA  
AAGGACAGTCACATTGCTCAAAGNACTCAAGTTTAGCCCGAGTACAGTAGCT {(SEQ  
ID NO:100)}

Genbank ID: Z24212

Description: H. sapiens (D18S477) DNA segment containing (CA) repeat; clone

Search for GDB entry

D18S979:

Database ID: GATA-P28080 (Also known as G08015, CHLC.GATA92C08, CHLC.GATA92C08.P28080)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats

Chromosome: Chr18

Primers:

Left = AGCTTGCAGATAGCCTGCTA {(SEQ ID NO:101)}

Right = TACGGTAGGTAGGTAGATAGATTCG {(SEQ ID NO:102)}

Product Length = 155

Review complete sequence:

CTCTACAGTCTCTNACCTTTGGACTCCAGGACTTTCACCAGCACCTCAACATTCCCA  
CTGGGTTCTCAGGACTTTATAGTTGTACTGAGCCATGCCACTGGATCCTAGGGTCTC  
CAGCTTGCAGATAGCCTGCTATGGGACTTAATCTTTGTAATAAGGTGAGTCAATTCT  
GCCAATAAACCTACTTTCATCTCTATCTATCTATCTATCTATCTATCTATCTATA  
TCTATCATCTATCTATCGAATCTATCTACCTACCTACCGTATTAGTTCTGTCTCTCTGG  
AGN {(SEQ ID NO:103)}

Genbank ID: G08015

Description: human STS CHLC.GATA92C08.P28080 clone GATA92C08.

WI-9340:

Database ID: UTR-05134 (Also known as G06102, D18S1034, 9340, X60221)

Source: WICGR: Primers derived from Genbank sequences

Chromosome: Chr18

Primers:

Left = TGAGAGAACGAAATCTCTATCGG {(SEQ ID NO:104)}

Right = AGGCAGCAAGTTTTATAAAGGC {(SEQ ID NO:105)}

Product Length = 115

Review complete sequence:

ATGTATCTATCCCAATTGAGTCAGCTAGAAACAGTTGACTGACTAAATGGAACTAG  
TCTATTTGACAAAGTCTTTCTGTGTTGGTGTCTACTGAAGTTATAGTTTACCCTTCCT  
AAAAATGAAAAGTTTGTTCATATAGTGAGAGAACGAAATCTCTATCGGCCAGTCA  
GATGTTTCTCATCCTTCTTGCTCTGCCTTTGAGTTGTTCCGTGATCATTCTGAATAAG  
CATTTGCCTTTATAAAAACTTGCTGCCTGACTAAAGATTAACAGGTTATAGTTTAAA  
TTTGTAATTAATTCTACCATCTTGCAATAAAGTGACAATTGAATG {(SEQ ID NO:106)}

Genbank ID: G06102

Description: WICGR: Random genome wide STSs

Search for GDB entry

D18S466:

Database ID: AFM094YE5 (Also known as 094ye5, Z23354, D18S466)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs  
Chromosome: Chr18

Primers:

Left = ACACTGTAGCAGAGGCTTGACC {(SEQ ID NO:107)}

Right = AGGCCAAGTTATGTGCCACC {(SEQ ID NO:108)}

Product Length = 214

Review complete sequence:

aaatgacactttaaggaggtaacactgtagcagaggcttgaccaccaccagttctactagcactgaggatgctctattgggtgggttacc  
acacacgcatagacatgcacacacagacacacagacacacacacacacacacaccagatatagcattccaaacctcaatatgc  
tatgcaatactgcattaacaggtcatgcctgtggtggcacataactggcctagaaaatactggggacgtctgcattccctttattatcgaattg  
acttacttggtctctgagtttctcagaagtaacttcaatacctctccattctgccttgancattgttgggtaccaagtatagct {(SEQ  
ID NO:109)}

Genbank ID: Z23354

Description: H. sapiens (D18S466) DNA segment containing (CA) repeat; clone

Search for GDB entry

D18S1092:

Database ID: AFMA112WE9 (Also known as D18S1092, w5374, a112we9)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = CTCTCAAAGTAAGAGCGATGTTGTA {(SEQ ID NO:110)}

Right = CCGAAGTAGAAAATCTTGGA {(SEQ ID NO:111)}

Product Length = 163

Review complete sequence:

agctctcaaagtaagagcgatgttgtaactgactgagttgtttgtgaantttgntttggagtcagtgaggcatgttattagatgtaaattaaac  
acacacacacacacacacacacacacacagagaagtaagtccaagattttacttcggcgccctatattctatatactgattttctgtatttc  
ccagacttgaatatagattgtctttctgntttatcatagacaatctcataaanttaggcataataaggtaatgaggntttctgggcttctttcat  
catccctgcaattgagctctntttatagntgaantcttctctgtaataacntctgttttagct {(SEQ ID NO:112)}

Search for GDB entry

D18S61:

Database ID: AFM193YF8 (Also known as 193yf8, Z16834, D18S61)

Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:

Left = ATTTCTAAGAGGACTCCCAAAC {(SEQ ID NO:113)}

Right = ATATTTTGAAACTCAGGAGCAT {(SEQ ID NO:114)}

Product Length = 174

Review complete sequence:

CGTCTTACCAAACCAACATAATATAGCAATGGNAACCAAAAAATTTCTAAGAG  
GACTCCCAAACTACATTCTTCTNCCTGAATTAAATACAGGCATTCAANANAAACANA  
CACACACACACACACACACACACACACACACACACGCACACCCTTCAAATCNTA  
GCATAAATTCCNCTTATATAAACATAACCATGCTCCTGAGTTTCAAAATATTGGGTG  
GTTCTGAAGTTCGAAGCAACAAATTTCCAGTTAGTGTCTATTANTTGTGGACAGCT  
{(SEQ ID NO:115)}

Genbank ID: Z16834

Description: *H. sapiens* (D18S61) DNA segment containing (CA) repeat; clone

## Search for GDB entry

**Markers (STRs) used in refining the candidate region.**

Below the markers are shown that were used in family MAD31 to refine the candidate region. Most of these markers are already described above and will therefore only be mentioned to by their name. For the additional markers, the information is given here.

Data was already shown for: D18S68, D18S55, D18S969, D18S1113, D18S483, D18S465, D18S876, D18S477, D18S979, D18S466 and D18S61.

New data:

D18S51:

Other names: UT574, (D18S379)

Primer sequences:

UT574a GAGCCATGTTCATGCCACTG {(SEQ ID NO:116)}

UT574b CAAACCCGACTACCAGCAAC {(SEQ ID NO:117)}

DNA-sequence:

AATTGAGCNCAGGAGTTTAAAGACCAGCCTGGGTAACACAGTGAGACCCCTGT  
CTCTACAAAAAATACAAAAATNAGTTGGGCATGGTGGCACGTGCCTGTAGTCTCA  
GCTACTTG CAGGGCTGAGGCAGGAGGAGTTC TTGAGCCCAGAAGGTTAAGGCTGCA  
GTGAGCCATGTTCATGCCACTGCACTTCACTCTGAGTGACAAATTGAGACCTTGTCT  
CAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAANGAAAGAAAGAAA  
GTAAGAAAAAGAGAGGGAAAGAAAGAGAAANAGNAAANAATAAGTAGCAACTGTT  
ATTGTAAGACATCTCCACACACCAGAGAAGTTAATTTTAATTTTAACATGTTAAGAA  
CAGAGAGAAGCCAACATGTCCACCTTAGGCTGACGGTTTGTTTATTTGTGTTGTTGC  
TGGTAGTCGGGTTTGTTATTTTTAAAGTAGCTTATCCAATACTTCATTAACAATTTCA  
GTAAGTTATTTTCATCTTTCAACATAAATACGNACAAGGATTTCTTCTGGTCAAGACC  
AAACTAATATTAGTCCATAGTAGGAGCTAATACTATCACATTTACTAAGTATTCTAT  
TTGCAATTTGACTGTAGCCCATAGCCTTTTGTCGGCTAAAGTGAGCTTAATGCTGATC  
GACTCTAGAG {(SEQ ID NO:118)}

GENBANK ID: L18333

D18S346.

Other name: UT575

Primer Pairs:

Primer A: TGGAGGTTGCAATGAGCTG {(SEQ ID NO:119)}

Primer B: CATGCACACCTAATTGGCG {(SEQ ID NO:120)}

DNA sequence:

ACGAGGACAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCCCGTTTNTACTA  
AAANTACAAAANTTGGTCGGGAGGCTGGGGCAGGNGACATGCTTGACCCCAGGAGG  
TGGAGGTTGCAATGAGCTGAGATTGCACCACTGCACTNCAGCNTGG. {(SEQ ID  
NO:121)}.....AAGAAAGAGAAAGGANAGNNAGGNAGNNANNAAACTACATNTGAAGT  
CAACACTAGTATTGGTGGGAGAGGAATTTTATGCTGCATTCCCNACAACCACTAGA  
TACGCCAATTAGGTGTGCATGGTCCATGCTAT {(SEQ ID NO:122)}

GenBank ID: L26588

D18S817.

Other name: UT6365

Primer Pairs:

Primer A: GCAAAGCAGAAGTGAGCATG {(SEQ ID NO:123)}

Primer B: TAGGACTACAGGCGTGTGC {(SEQ ID NO:124)}

DNA Sequence:

CATATGGGTCCACAAGCAACCTCAGTCCTTGTCTCTTCAGAAGAAAGAATTCTACTG  
AGGGNCATAAAGCAGAAGGAGAGACCTAGGCAAGTTGCAAAGCAGAAGTGAGCAT  
GTATTA AAAAGCTTTAGAACAGTAAGGAAAGGAAGAAAAGAAAAGAAGGAAAGTT  
CAACTTGGAAGAGGGCCAAGCCGGCAACTTGGCAGAAGGATTGCTTGAGCCCAGGA  
GTTAAGACCAGTCTGGGCAATATAGTGAGACTCCATCTCTGCATACATACATACATA  
CATACATACATACATACATACATATTCAGGGTATGATGGCACACGCCTGTAG  
TCCTAGCTACTCTGGAGGTTGAGATGGGAGGGTCACTGAGCCTGGGAANTTGAGGC  
TGCNNTGAGCCATGATC {(SEQ ID NO:125)}

GenBank ID: L30552

**Characterisation of YACs.**

8 YACs were selected covering the candidate region and flanking the gap. These YACs were further characterised by determining the end-sequences by the Inverse-PCR protocol.

Selected YACs: 961\_h\_9, 942\_c\_3, 766\_f\_12, 731\_c\_7, 907\_e\_1, 752\_g\_8, 717\_d\_3, 745\_d\_2

New STSs based on end-sequences (unless indicated otherwise, the STSs were tested on a monochromosomal mapping pannel for identifying chimaerism of the YAC; if the STS revealed a hit not on chromosome 18q -chimaeric YAC- then it is indicated in the text below):

#### SV32L.

Derived from YAC 745\_d\_2 left arm end-sequence.

Primer A: GTTATTACAATGTCACCCTCATT {(SEQ ID NO:126)}

Primer B: ACATCTGTAAGAGCTTCACAAACA {(SEQ ID NO:127)}

DNA-sequence:

ATTCCTTNGTTATTACAATGTCACCCTCATTTAAAAAGTGGAAGATAAAGAGGAAG  
CAATCTATTTTTTCTTTTTTCTGATAGCACTTGTTTGTGAAGCTCTTACAGATGTT  
CTTAAGTAAAATCAACTCCTCCATTTTTTTGTAGCAACTACACATATTTATCAATAA  
TAGTTCACAAATACATTTTCAAATT {(SEQ ID NO:128)}

Amplified sequence length: 107 basepairs (bp)

This STS has no clear hit on the monochromosomal mapping pannel.

#### SV32R.

Derived from YAC 745\_d\_2 right arm end-sequence.

Primer A: ACGTTTCTCAATTGTTTAGTC {(SEQ ID NO:129)}

Primer B: TGTCTTGGCATTATTTTAC {(SEQ ID NO:130)}

DNA sequence:

AGACAATGGGAGAAATTGCACTGCCCTGAGTCAGAAATCAGATCTGTTGCCATACA  
GCTGCCGTTATGTGATCATTTGCAAGTCAACGTTTCTCAATTGTTTAGTCATTTGTAA  
GACAAAAAGACTGGTTGGATTTAGAGAAATTTGGAATCCTCCTTCAGGTTTAAACAAG  
CAATAAATGATACTCTTCAGTGTAATAATAATGCCAAGACATNATTTGACTTTAAAT  
TAAATCCAAACAAGATATC {(SEQ ID NO:131)}

Amplified sequence length: 127 bp

This STS has no clear hit on the monochromosomal mapping pannel.

SV11L.

Derived from YAC 766\_f\_12 left arm end-sequence.

Primer A: CTATGCTCTGATCTTTGTTACTTT {(SEQ ID NO:132)}

Primer B: ATTAACGGGAAAGAATGGTAT {(SEQ ID NO:133)}

DNA sequence:

GTCTTTATTTTCATATAACTATGCTCTGATCTTTGTTACTTTCTCCTTTTAACTCAGTTT  
AAGCTTTATTCTTATTTTCCAGCTGCTGAAGGTATATAGTTAGGTTGTTTATTGGATA  
CCATTCTTTCCCGTTAATGTCAGTGGTACTGCTATCAATGTAGCAGTTA {(SEQ ID  
NO:1)}

Amplified sequence length: 118 bp

This STS has a hit with chromosome 18 and must be located between CHLC.GATA-p6051 and D18S968.

SV11R.

Derived from YAC 766\_f\_12 right arm end-sequence.

Primer A: AAGGTATATTATTTGTGTCG {(SEQ ID NO:134)}

Primer B: AAACCTTTCTTAACCTCATA {(SEQ ID NO:135)}

DNA sequence:

ATAAGGTATATTATTTGTGTCGTGAGTTAAGAAATCATTAATAACTATTTTCAGAAT  
GACAAATGTCATTATATGTTGTAAAAAAGATAAATACGTGAAATTATGAGGTTAAG  
AAAAGTTTA {(SEQ ID NO:2)}

Amplified sequence length: 119 bp.

This STS has a hit with chromosome 18 and must be located between D18S876 and GCT3G01.

SV34L.

Derived from YAC 717\_d\_3 left arm end-sequence.

Primer A: TCTACACATATGGGAAAGCAGGAA {(SEQ ID NO:136)}

Primer B: GCTGGTGGTTTTGGAGGTAGG {(SEQ ID NO:137)}

DNA sequence:

ACATAAAATGTCGCTCAAAAACAATTATGTGTGTCTACACATATGGGAAAGCAGGA  
AACAAATTTGTTTACAACATACATTACTTTTGTTTTTTAGGCAAGATAAAATNTCCTA  
CCTCCAAAACCAACGACACNGTCCGCAATAACTATACATC {(SEQ ID NO:3)}

Amplified sequence length: 98 bp

This STS has a hit with chromosome 18.

#### SV34R.

Derived from YAC 717\_d\_3 right arm end-sequence.

Primer A: ATAAGAGACCAGAATGTGATA {(SEQ ID NO:138)}

Primer B: TCTTTGGAGGAGGGTAGTC {(SEQ ID NO:139)}

DNA-sequence:

AATATCATTCTTCACCCACGTTATACATAAGAGACCAGAATGTGATATTGTCATCTC  
ACATGGAAAAATCTGCTGTGATCAGTTCCTGAAGCTTGCTGTGATCCTCCCTTAGGA  
AAGTAGAAAAATCTTTTTGAAACACTTTATTCTACAATCAATGAAAATTAGGTGAAG  
CTACAGAAGCCAGAAATTACTCTAAGATTAGACAATTATTTAAGANGACCAATTGTC  
TTTGGTCTTCTTCTGAAGGGTCTGACTACCCTCCTCCAAAGAATTCACTGGCCGTCGT  
TTTACAACGTCNTGA {(SEQ ID NO:4)}

Amplified sequence length: 244 bp

This STS has a hit with chromosome 1, therefore YAC 717\_d\_3 is chimaeric

#### SV25L.

Derived from YAC 731\_c\_7 left arm end-sequence.

Primer A: AAATCTCTTAAGCTCATGCTAGTG {(SEQ ID NO:140)}

Primer B: CCTGCCTACCAGCCTGTC {(SEQ ID NO:141)}

DNA sequence:

AGTGGAGAGATAGAAAGAGAGGAAGATTTTTTTTTTTAAATCTCTTAAGCTCATGCT  
AGTGTAGGTGCTGGCAGGTCTGAACACTCTGTAGGACAGGCTGGTAGGCAGGAA  
{(SEQ ID NO:142)}

Amplified sequence length: 72 bp



This STS has no clear hits on the monochromosomal mapping pannel.

SV25R.

Derived from YAC 731\_c\_7 right arm end-sequence.

Primer A: TGGGGTGCCTGTGTTGT {(SEQ ID NO:143)}

Primer B: GAGATTTTCATGCATTCCTGTAAGA {(SEQ ID NO:144)}

DNA-sequence:

GGAGGGTGTNTCACANAAGTCTGGGGTGCCTGTGTTGTTTCATTGTAAAAACCCTT  
TGGANCATCTGGGAATGTGCTGCCCCACATGTCCAGGTAACGTTCTCAGGAAGGGG  
AGGCTGGAAATCTCTGTGTGTTCTTACAGGAATGCATGAAATCTCCCANCCCCCTCTT  
GTTGGAAATTTCCCTCACTTT {(SEQ ID NO:5)}

Amplified sequence length: 136 bp

This STS has a hit with chromosome 7; therefore YAC 731\_c\_7 is chimaeric

SV31L.

Derived from YAC 752\_g\_8 left arm end-sequence.

Primer A: GAGGCACAGCTTACCAGTTCA {(SEQ ID NO:145)}

Primer B: ATTCATTTTCTCATTTTATCC {(SEQ ID NO:146)}

DNA-sequence:

CTTCTCNATGANTGGACAAATGTCATTGGGTCAGCATGAGGCACAGCTTACCAGTTC  
AGATTCCAGTAGCTGAGGAACAAATCTTAACCTCAAAAATAAGTAATTGCGTCACTT  
TGGAGGAATTATTTGACCTTTTCATAACTTTGACATCACAACAATGAGGGTGAAGTT  
AGTAAAATAAATGATTATTATGAGGATAAAATGAGAAAATGAATTNAGTGCTTAAG  
ACAATGCTTGGTAACTAGTTAANCCG {(SEQ ID NO:6)}

Amplified sequence length: 178 bp

This STS has a hit with chromosome 18 and must be located between D18S876 and GCT3G01.

SV31R.

Derived from YAC 752\_g\_8 right arm end-sequence.

Primer A: CAAGATTATGCCTCAACT {(SEQ ID NO:147)}

Primer B: TAAGCTCATAATCTCTGGA {(SEQ ID NO:148)}

DNA sequence:

AAACTTTAACCAATTTAAACTCCCTAACAGTTCTATAAAATAAGCAAGATTATGCCT  
CAACTTTATGGATAAAGAAATGGAGGCATTAAGAGATAACTAACTTGCCCAAGGCC  
ACACAAGTGACTGAGTAAGAATTGCAAAGCCAATGAGTCTGGCTCCAGAGATTATG  
AGCTTAATCACCACACTGTGCCACCTCCTGTGTTTCCTGG {(SEQ ID NO:149)}

Amplified sequence length: 131 bp

This STS has no clear hits on the monochromosomal mapping pannel and gives no information concerning the chimaerity of the YAC.

#### SV10L.

Derived from YAC 942\_c\_3 left arm end-sequence.

Primer A: TCACTTGGTTGGTTAACATTACT {(SEQ ID NO:150)}

Primer B: TAGAAAAACAGTTGCATTTGATAT {(SEQ ID NO:151)}

DNA-sequence:

GGTNTTTCACCTTGGTTGGTTAACATTACTTCTAAGTTTTTTATTGTTTTTTATGCTATT  
GCTAATGGGATTGCTTTCTTAATTTATTTTTTCCAATAGCTTGTTGTTAGTTTATATCA  
AATGCAACTGTTTTTCTATGCAAATTATGTTTCCT {(SEQ ID NO:7)}

Amplified sequence length: 130 bp

This STS has a hit with chromosome 18 and must be located between CHLC.GATA-p6051 and D18S968

#### SV10R.

Derived from YAC 942\_c\_3 right arm end-sequence.

Primer A: AACCCAAGGGAGCACAACTG {(SEQ ID NO:152)}

Primer B: GGCAATAGGCTTTCCAACAT {(SEQ ID NO:153)}

DNA sequence:

TTGGTGGTGCCCTAGGTTTGGCAATTATAAATAAAGCTGCTACAAACATTCATGTGC  
AGGTCTCCGTGTGGACATAATTTCCAGTTCATTTGGGTAAAACCCAAGGGAGCACACA  
ACTGTTGGATCCTATNATAAAAAATATNTCTCGTTTCATTTAACCTGGGAAACT  
ATCTNCCCACAGTGGCTGTCCCTTTTGTATCCCCACCAACAATGTTGGAAAGCCTAT  
TGCCANCAT {(SEQ ID NO:8)}

Amplified sequence length: 135 bp

This STS has a hit with chromosome 18 and must be located between D18S876 and GCT3G01

SV6L.

Derived from YAC 961\_h\_9 left arm end-sequence.

No primer was made, because this sequence is identical to a known STR marker D18S42, which is indeed mapped to this region.

Primer A:

Primer B:

DNA sequence:

CATGNCTCACAGTGTCTGAGGCTGCTCTGGACATGCAATCTTGCATGCTTTTGTCAT  
GACAGGTCTTAAANAGTTTATCAGCTTNCTCAAATAGCTGAATGACANAACACTGG  
ATTTTGTTCAAATANCCTATCAACTTGGCNTCTGTGTTGCGGTTGTCACTTGGTAAC  
AAAATAAGTC {(SEQ ID NO:9)}

Amplified sequence length:

SV6L recognises D18S42 which must be therefore located between WI-7336 and WI-8145

SV6R.

Derived from YAC 961\_h\_9 right arm end-sequence.

Primer A: TTGTGGAATGGCTAAGT {(SEQ ID NO:154)}

Primer B: GAAAGTATCAAGGCAGTG {(SEQ ID NO:155)}

DNA sequence:

TAATTGACAAATAAAAATTGTATATTTTNCATATTTAACATGTTATGCTAACATATAT  
ATGGATTGTGGAATGGCTAAGTCAGAAATTCCTTTACATTCATATTTCCATATTATTT  
ACTTTNNGCTTTAAAAAATATGTAAATGANAATACTTATTTTTTTTCAGTGTCACTGCC  
TTGATACTTTTACATTTNNGTTACATATTATTTCCCTTNCATCTAACAAATATATATT  
GAGTTTCTATAATGTGTCTGACACTGA {(SEQ ID NO:10)}

Amplified sequence length: 122 bp

SV6R amplifies a segment on chromosome 18. This segment must be located between WI-2620 and WI-4211

### SV26L.

Derived from YAC 907\_e\_1 left arm end-sequence.

Primer A: TATTTGGTTTGTGCTGAGGT {(SEQ ID NO:156)}

Primer B: CAAGAAGGATGGATACAAACAAG {(SEQ ID NO:157)}

DNA sequence:

TGGTCACTGGTGCCTTTATTTGGTTTGTGCTGAGGTCATATTCCTGTGGCCTTCAT  
GCTTGATTTGTTGGAGTCTAGCCATGTAAAANTCTGTTGGAGTCTAGGCATTAAAA  
AATAGGTATTTATTGTAATCTTTGCCATTTGCTTGTTTGTATCCATCCTTCTTGGGAA  
GGCTTTACAGGCATTCAAAGG {(SEQ ID NO:11)}

Amplified sequence length: 154 bp

This STS has a hit with chromosome 13; therefore YAC 907\_e\_1 is chimaeric.

### SV26R.

Derived from YAC 907\_e\_1 right arm end-sequence.

Primer A: CGCTATGCATGGATTTA {(SEQ ID NO:158)}

Primer B: GCTGAATTTAGGATGTAA {(SEQ ID NO:159)}

DNA sequence:

CGCTATGCATGGATTTAAACTGAGTGTAGTGCCTCACTATGTTGCAGTCTCTTATTC  
TAGGTTCTTAATATTTACATCCTAAATTCAGCT {(SEQ ID NO:160)}

Amplified sequence length: 90 bp

no clear hits on monochromosomal mapping pannel: no information concerning chaemerity at this side of the YAC

### **Page 64, line 5 through line 19:**

A 4.5kb ECORI/Sall fragment of pBLC8.1 (Lewis *et al*, 1992) carrying a lysine-2 and a telomere sequence was directionally cloned into GEM3zf(-) digested with ECORI/Sall.

Subsequently, an End Rescue Site was ligated into the EcoRI site. Hereto, two oligonucleotides (strand 1: 5'-TTCGGATCCGGTACCATCGAT-3' {(SEQ ID NO:161)} AND STRAND 2: 3'GCCTAGGCCATGGTAGCTATT-5' {(SEQ ID NO:162)}) were ligated into a partial (dATP) filled ECORI site, generating the vector pDF1. Triplet repeat containing fragmentation vectors were constructed by cloning of a 21bp and a 30bp CAG/CTG adapter into the Klenow-filled PstI site of pDF1. [Trasformation] Transformation and selection resulted in a (CAG)<sub>7</sub> and a (CTG)<sub>10</sub> fractionation vector with the orientation of the repeat sequence 5' to 3' relative to the telomere.